

C parts individually contribute at least one but less than eleven bases to said triple stranded complex.--

REMARKS

Reconsideration and withdrawal of the rejections made in the March 10, 2000 Office Action is respectfully requested in view of the above amendments and the following comments.

Claims 31-85 were rejected under 35 USC §112, first paragraph, as containing new matter. Claims 31-85 have been canceled and new claims added to the application which do not contain the language "aggregate" and "aggregate binding regions". As discussed in applicants prior response, this language was intended to indicate that molecule C could be in more than one part. In other words, molecule C is not required to be one continuous strand which binds to nucleic acid A. Molecule C could have several different parts which bind to different regions of nucleic acid A. This is clear from figures 3 and 4 which show more than one molecule C parts (i.e. molecules with different sequences which bind to different parts of nucleic acid A). As shown in figures 3 and 4, all parts of molecule C which participate in the triple stranded complex bind to molecule A at the same time. In other words, "strand C" of the triple stranded complex may be composed of several parts or an aggregate. The new claim language is believed

to clarify this issue. In view of the cancellation of claims 31-85 and the addition of new claims to the application, applicants request that this rejection be withdrawn.

If new claims 86-\*\* are not entered, applicants respectfully contend that the language "aggregate" and "aggregate binding region" are not new matter. Though these terms do not specifically appear in the originally filed specification, there is no requirement that the words in a claim must exactly match those used in the specification [MPEP §2173(e)]. All that is required is that the application reasonably convey to persons skilled in the art that , as of the filing date the inventor had possession of the subject matter later claimed by him. In the present situation, figure 3 and 4 clearly show an aggregate (i.e. more than one) of molecule C. The term "aggregate" is generally used to mean "more than one unit taken as a whole", " a whole sum or amount", or "considered as a whole". Such language is clearly supported by the present application which shows more than one molecule C binding to nucleic acid A. When reading claim 31, it is clear that this language is used to convey that the one or more nucleic acid binding probes C considered as a whole or collectively comprise a base sequence different from the base sequence of nucleic acid binding probe B. Since nucleic binding probe C can be in more than one part, it is important that all of the parts be considered as a whole. The use of the phrase "in the aggregate" in claim 31 is intended to indicate that the comparison of the base sequence of nucleic acid A binding probe B should be made with the base sequence of all of the parts of probe C and not with each individual part of probe C (i.e. the aggregate base sequence). Figures 3, 4

and 10 and pages 16-18 of the present application support this language and describe the formation of such complexes as well as how the base sequences of the two or more nucleic acid A binding probes C must interact with nucleic acid A and the nucleic acid A binding probe B to form many variations of the complex. Even paragraph 4 of the present Office Action admits that the present specification describes a triple stranded binding region with two independent probes C1 and C2. In view of the disclosure in the present application, applicants respectfully contend that one skilled in the art would clearly understand the meaning and scope of the claims which use the language "in the aggregate" based on the generally accepted definition and the disclosure in the present application.

Regarding the term "aggregate binding region", applicants contend that the present application clearly supports a collection of binding regions of probe C. Figures 3, 4 and 10 of the present application show two separate parts of probe C which clearly have different binding regions. Thus the language "aggregate binding region" refers to the binding regions of all of the parts of probe C. The Office Action contends that it is unclear as to whether the aggregate binding region is on nucleic acid A or probe C. Since claims 31-85 clearly indicate that there can be more than one probe C, the term "aggregate binding region" clearly applies to probe C. Regarding the physical and chemical features which define the aggregate binding region, figures 3, 4 and 10 and pages 16-18 of the present application would lead one skilled in the art to the conclusion that the "aggregate binding region" is the base sequence of the one or more nucleic acid A binding probes C that bind with nucleic acid A and participate in forming the claimed triple

stranded complex with nucleic acid A binding probe B. One skilled in the art would know that a triple helix is formed from hydrogen bonding of nucleobase containing subunits of the component polymers and that the triple stranded complex is comprised of the component binding regions of each of the component polymers that hybridize and assemble to form the double and triple helix structures taught in the present application. Since there can be two or more nucleic acid A binding probes C, it is clearly the aggregate binding region of the two or more nucleic acid binding probes C which together must bind nucleic acid A and participate in the formation of the triple stranded complex of the present invention. In view of the above discussion, applicants contend that the terms "aggregate" and "aggregate binding region" are not new matter and request that this rejection be withdrawn.

Claims 31-85 were rejected under 35 USC §112, second paragraph as indefinite regarding the terms "aggregate" and "aggregate binding region". Claims 31-85 have been canceled and new claims added with do not include this language . In view of the cancellation of claims 31-85 applicants request that this rejection be withdrawn. If the new claims are refused entry, applicants contend that the terms "aggregate" and "aggregate binding region" are not indefinite in view of the above discussion of these terms regarding the new matter rejection.

Claims 31, 32, 34-36, 42-43, 55, 56, 58, 63-64, 69, 70 and 72 were rejected under 35 USC §102(b) as anticipated by Svinarchuk. As discussed above, claims 31-85 have been canceled and new claims added to the application. The new claims indicate that the triple stranded complex is more thermostable than a triple

stranded complex formed from either of: (a) two nucleic acid A binding probes B binding with one nucleic acid A; or (b) two of said nucleic acid A binding probes C binding with one nucleic acid A. Svinarchuk is directed to compositions which form using a single probe which binds to a double stranded nucleic acid to form a triplex. The claims of the present application all require the use of two probes (B and C) to form the triple stranded complex which is then detected. Svinarchuk does not suggest or disclose that the triple stranded complex is more thermostable than a triple stranded complex formed from either of: (a) two nucleic acid A binding probes B binding with one nucleic acid A; or (b) two of said nucleic acid A binding probes C binding with one nucleic acid A and thus does not anticipate the present claims.

In addition, applicants point out that Svinarchuk does not disclose all of the limitations to claims 31-85. The Office Action correctly states that Svinarchuk teaches a double stranded molecule with a [single] probe hybridized to a specific region (page 5 of the Office Action). However, page 4 of the Office Action refers to a binding probe B and a binding probe C when discussing Svinarchuk. This is incorrect as Svinarchuk uses a double stranded nucleic acid and a single probe. Though Svinarchuk results in a triple stranded complex, his method does not involve two binding probes.

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Respectfully submitted,

Arent Fox Kintner Plotkin & Kahn



Monica Chin Kitts

Attorney for Applicants

Registration No. 36,105

Atty. Docket No. P8382-8067

1050 Connecticut Avenue, N.W.

Suite 600

Washington, D.C. 20036-5339

(202) 857-6000

MCK/mck